



SEQUENCE LISTING

<110> Walker, Ameae M.

<120> PROLACTIN ANTAGONISTS AND USES THEREOF

<130> Walker_2500_097US2

<140> 09/065,330

<141> 1998-04-23

<150> PCT/US97/01435

<151> 1997-01-30

<150> 08/594,809

<151> 1996-01-31

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 832

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (622)..(624)

<223> This is the codon for the substituted amino acids
of the mutated sequence.

<400> 1

aacatgaaca	tcaaaggatc	gccatggaaa	gggtccctcc	tgctgctgct	ggtgtcaaac	60
ctgctgctgt	gccagagcgt	ggcccccttg	cccatctgtc	ccggcggggc	tgcccgatgc	120
caggtgaccc	ttcgagacct	gtttgaccgc	gccgtcgtcc	tgtcccacta	catccataac	180
ctctcctcag	aaatgttcag	cgaattcgat	aaacgggtata	cccatggccg	ggggttcatt	240
accaaggcca	tcaacagctg	ccacacttct	tcccttgcca	ccccgaaga	caaggagcaa	300
gccaacaga	tgaatcaaaa	agactttctg	agcctgatag	tcagcatatt	gcgacccctg	360
aatgagcctc	tgtatcatct	ggtcacggaa	gtacgtggta	tgcaagaagc	cccggagggt	420
atcctatcca	aagctgtaga	gattgaggag	caaaccacaa	ggcttctaga	gggcatggag	480
ctgatagtca	gccagggttc	tcctgaaacc	aaagaaaatg	agatctaecc	tgtctgggtc	540
ggacttccat	ccctgcagat	ggctgatgaa	gagtctcgcc	tttctgctta	ttataacctg	600
ctccactgcc	tacgcaggga	tnnncataaa	atcgacaatt	atctcaagct	cctgaagtgc	660
cgaatcatcc	acaacaacaa	ctgctaagcc	cacatccatt	tcatctatct	ctgagaaggt	720
ccttaatgat	ccgttccatt	gcaagcttct	tttagttgta	tctcttttga	atccatgctt	780
gggtgtaaca	ggtctcctct	taaaaaataa	aaactgactc	gtagagaca	tc	832

<210> 2
<211> 228
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (208)
<223> Site mutated codon where the normal codon coding
for serine is modified preferably to encode for
aspartate or glutamate, most preferably aspartate.

<400> 2
Asn Met Asn Ile Lys Gly Ser Pro Trp Lys Gly Ser Leu Leu Leu Leu
1 5 10 15
Leu Val Ser Asn Leu Leu Leu Cys Gln Ser Val Ala Pro Leu Pro Ile
20 25 30
Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu Arg Asp Leu Phe
35 40 45
Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn Leu Ser Ser Glu
50 55 60
Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly Arg Gly Phe Ile
65 70 75 80
Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu Ala Thr Pro Glu
85 90 95
Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp Phe Leu Ser Leu
100 105 110
Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu Tyr His Leu Val
115 120 125
Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala Ile Leu Ser Lys
130 135 140
Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu Glu Gly Met Glu
145 150 155 160
Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu Asn Glu Ile Tyr
165 170 175
Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala Asp Glu Glu Ser
180 185 190

Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu Arg Arg Asp Xaa
195 200 205

His Lys Ile Asp Asn Tyr Leu Lys Leu Leu Lys Cys Arg Ile Ile His
210 215 220

Asn Asn Asn Cys
225

<210> 3
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: This sequence
is a primer.

Ci <400> 3
gcagggatga ccacaagggtt gac

23

<210> 4
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: This sequence
is a primer.

<220>
<221> variation
<222> (12)
<223> This is a codon that can be replaced for nucleic
acid substitutes.

<400> 4
cgcaagggat gnacacaagg ttga

24

<210> 5
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: This sequence
is a primer.

<220>
<221> variation
<222> (12)
<223> This is a codon that can be replaced for nucleic
acid substitutes.

CI <400> 5
acgcagggat gnkataaaat cg

22

<210> 6
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: This sequence
is a primer.

<400> 6
cgtggccccc atatgttgcc catctg

26